

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 18, 2002, 02:17:48 ; Search time 733.22 Seconds
(without alignments)
1847.529 Million cell updates/sec

Title: US-09-719-748-1_COPY_98_886

Perfect score: 789

Sequence: 1 tatgacacgcgagagagctcctcagacacccctgagtc 789

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N.Geneseq_033802.*
1: /net/abs06/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/NA1980.DAT.*
2: /net/abs06/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/NA1981.DAT.*
3: /net/abs06/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/NA1982.DAT.*
4: /net/abs06/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/NA1983.DAT.*
5: /net/abs06/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/NA1984.DAT.*
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11: /net/abs06/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/NA1990.DAT.*
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16: /net/abs06/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/NA1995.DAT.*
17: /net/abs06/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/NA1996.DAT.*
18: /net/abs06/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/NA1997.DAT.*
19: /net/abs06/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/NA1998.DAT.*
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21: /net/abs06/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/NA2000.DAT.*
22: /net/abs06/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/NA2001A.DAT.*
23: /net/abs06/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/NA2001B.DAT.*
24: /net/abs06/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	789	100.0	1742	21	AA249765 Human DAP-kinase-r
2	760.2	96.3	1253	23	AA573461 DNA encoding novel
3	495.2	62.8	2079	22	AAK94258 Human full-length
4	494.6	62.7	1439	20	AAK34657 Murine ZIP-kinase
5	493.6	62.6	2132	20	AAK34656 Human ZIP-kinase (
6	493.6	62.6	2224	22	AAH16158 Human cDNA sequenc
7	493.6	62.6	2224	22	AAH78068 Nucleotide sequenc
8	398.2	50.5	4272	16	AA089839 Human death associ
9	398.2	50.5	5886	16	AA089838 Human death associ

10	398.2	50.5	5886	19	AAV60289 DNA sequence encod
11	366.6	46.5	757	22	AAK91856 Human cDNA 5'-end
12	366.6	46.5	757	22	AAK93262 Human cDNA clone r
13	244.6	31.0	12638	22	AAK70641 Human Immune/haema
14	228.8	29.0	1120	22	ABAO9608 Human bone marrow
15	228.8	29.0	1505	22	ABAO9692 Human bone marrow
16	202.8	25.7	3192	21	AAH16067 Human prostate can
17	193.6	24.5	480	21	AAZ29731 cDNA encoding huma
18	193.6	24.5	1864	21	AAZ29730 cDNA encoding huma
19	187.2	23.7	873	22	AAH46902 cDNA encoding huma
20	176.6	22.4	1776	22	AAH4679 cDNA encoding huma
21	173	21.9	539	22	AAH06178 Human cDNA clone (
22	166.8	21.1	3284	23	ABH18303 Drosophila melanog
23	166.8	21.1	3374	23	ABH11987 Drosophila melanog
24	166.2	21.1	2562	23	ABH03417 Drosophila melanog
25	164.8	20.9	1836	22	AA506721 polynucleotide seq
26	164.8	20.9	2046	22	AAH09608 Nucleotide sequenc
27	163.8	20.8	2625	22	AAH4661 Novel protein kina
28	163.8	20.8	5532	20	AAZ25100 Human ischemic he
29	163.4	20.7	3864	22	AAH4664 Novel protein kina
30	163.4	20.7	5355	20	AAH89220 Seq ID No: 28 of W
31	163.4	20.7	5355	20	AAH89221 Seq ID No: 30 of W
32	163.4	20.7	5355	21	AAZ39404 Human Trad protein
33	163.4	20.7	5355	21	AAZ39405 Human Trad protein
34	163.2	20.7	1839	24	AAD26573 Human POLY4 cDNA.
35	162	20.5	2671	22	AAH4650 Novel protein kina
36	161.8	20.5	1971	24	AAH26571 Human POLY2 cDNA.
37	161.8	20.5	2558	24	AAH26572 Human POLY3 cDNA.
38	161.4	20.5	1917	23	ABH03333 Drosophila melanog
39	154	19.5	513	22	ABA60848 Human foetal liver
40	154	19.5	513	22	ABA28854 Probe #7320 for ge
41	154	19.5	513	22	AAK09135 Human brain expres
42	154	19.5	513	22	AAK35024 Human bone marrow
43	154	19.5	513	22	AAH16902 Probe #835 for ge
44	154	19.5	513	22	AAH40741 Probe #9427 used t
45	153.6	19.5	2973	24	AAH26453 Human kinase PKIN-

ALIGNMENTS

RESULT 1	AA249765	standard; DNA; 1742 BP.
AA249765	18-APR-2000	(first entry)
XX	AA249765;	
AC	AA249765;	
XX	18-APR-2000	(first entry)
DT	18-APR-2000	(first entry)
XX	Human DAP-kinase-related protein 1 (DRP-1) encoding DNA.	
DE	Human DAP-kinase-related protein 1 (DRP-1) encoding DNA.	
XX	DAP-kinase-related protein 1; DRP-1; Death-Associated Protein;	
KW	calmodulin-dependent serine/threonine kinase; apoptosis; dimerisation;	
KW	cytosolic; antiproliferative; immunosuppressive; metastasis; tumour; human;	
KW	treatment; cancer; psoriasis; autoimmune disease; screening; ds.	
XX		
OS	Homo sapiens.	
XX		
FT	Key	Location/Qualifiers
FT	CDS	62..1144
FT		/tag= a
FT		/product= "DAP-kinase-related protein 1"
FT		1720..1725
FT		/tag= b
XX		
XX		
PN	W09966030-A1.	
XX		
XX		
PD	23-DEC-1999.	
XX		
XX		
XX	15-JUN-1999;	99WO-US13411.
PF		
XX		
PR	15-JUN-1998;	98US-0089294.
XX		

PA (YEDA) YEDA RES & DEV CO LTD.
 PA (MCIN/) MCINNIS P A.
 XX Kimchi A;
 XX WPI: 2000-147148/13.
 DR P-PSDB: AAY44674.
 PT Calmodulin-dependent serine/threonine kinase capable of inducing
 XX apoptosis used in the treatment of e.g. cancer -
 XX
 PS Claim 3; Fig 1; 67pp; English.
 CC The present sequence encodes DAP (death-associated protein) -
 CC kinase-related protein 1 (DRP-1), which is a calmodulin-dependent
 CC serine/threonine kinase. DRP-1 is a cytoplasmic protein capable of
 CC inducing apoptosis by dimerisation. It shows significant homology to
 CC DAP kinase. It has cytosolic, antiproliferative and immunosuppressive
 CC activity and can be used for inhibiting growth/metastasis of
 CC tumours and promoting death of tumour cells. It can also be used in
 CC the treatment of cancer, psoriasis and autoimmune diseases. Fragments
 CC of DRP-1 DNA are useful as probes for screening individuals with a
 CC predisposition to cancer.
 XX
 SO Sequence 1742 BP; 442 A; 437 C; 504 G; 359 T; 0 other;

Query Match 100.0%; Score 789; DB 21; Length 1742;
 Best Local Similarity 100.0%; Pred. No. 1.5e-215;
 Matches 789; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tatgacatcgagagagagctggagagctggccagcttgcacatgtaagaagtcgagag 60
 DB 98 tatgacatcgagagagagctggagagctggccagcttgcacatgtaagaagtcgagag 157
 QY 61 aagagacggggcttgatgatcgagccaaagttcatcaagaagcgagagccggcgagc 120
 DB 158 aagagacggggcttgatgatcgagccaaagttcatcaagaagcgagagccggcgagc 217
 QY 121 cggcgcggtgtgagcggagagagatcgagcgggaggtgagatcctcgagagtgctg 180
 DB 218 cggcgcggtgtgagcggagagagatcgagcgggaggtgagatcctcgagagtgctg 277
 QY 181 caccacaatgcatcagcgtgacagcgtctatgagaacgcagcagcgtgtgtcacatc 240
 DB 278 caccacaatgcatcagcgtgacagcgtctatgagaacgcagcagcgtgtgtcacatc 337
 QY 241 ctgtgagctgtgtctggagagagctctgcttccctgcccagaagagagctgagtt 300
 DB 338 ctgtgagctgtgtctggagagagctctgcttccctgcccagaagagagctgagtt 397
 QY 301 gagagagagcaccagcgtctatcaagcagatcctgagtgagggtgaactcttcacaca 360
 DB 398 gagagagagcaccagcgtctatcaagcagatcctgagtgagggtgaactcttcacaca 457
 QY 361 aagaaatgtcgaactgtatctcaagcagaagaacatattgtttgtagacaagaattat 420
 DB 458 aagaaatgtcgaactgtatctcaagcagaagaacatattgtttgtagacaagaattat 517
 QY 421 cccattccacatcaagctgattgacttggcttgcgcacagaataagaatgagtt 480
 DB 518 cccattccacatcaagctgattgacttggcttgcgcacagaataagaatgagtt 577
 QY 481 gaattcaagaatatttttggagcgcggaattgtgtcccggaatttggactacagag 540
 DB 578 gaattcaagaatatttttggagcgcggaattgtgtcccggaatttggactacagag 637
 QY 541 cccctgggtctggagcgtacatgtgagcagatagcgctatacctaactctcttaagt 600
 DB 638 cccctgggtctggagcgtacatgtgagcagatagcgctatacctaactctcttaagt 697
 QY 601 ggagagctcccttctctggagagcagagcagaagcagaactgtgcaataatcagtagt 660

DB 698 ggagatcccttctctggagagacagcaggaagaacactgtgcaatatcacatcagtg 757
 QY 661 agtaagactttgtatggagatttctttagccatagcggagcgtggccaaagacttatt 720
 DB 758 agtaagactttgtatggagatttctttagccatagcggagcgtggccaaagacttatt 817
 QY 721 cggagacttctgtttaaagagaccgggaacgcgtccacatcaagaagagctctcagacac 780
 DB 818 cggagacttctgtttaaagagaccgggaacgcgtccacatcaagaagagagctctcagacac 877
 QY 781 cccctgagtc 789
 DB 878 cccctgagtc 886

RESULT 2
 AAS73461
 ID AAS73461 standard; CDNA; 1253 BP.
 XX
 AC AAS73461;
 DE 13-FEB-2002 (first entry)
 DE DNA encoding novel human diagnostic protein #9265.
 DE Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
 XX Homo sapiens.
 XX WO200175067-A2.
 XX 11-OCT-2001.
 XX 30-MAR-2001; 2001WO-US08631.
 XX 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX (HYSE-) HYSEQ INC.
 PA Drmanac RT, Liu C, Tang YT;
 DR WPI: 2001-639362/73.
 DR P-PSDB: ABG09274.
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensic, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 XX
 PS Claim 1; SEQ ID No 9265; 103pp; English.
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensic, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AAS64197-AAS94564 represent novel human
 CC diagnostic coding sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO

CC at fcp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 1253 BP; 331 A; 303 C; 366 G; 253 T; 0 other;

Query Match 96.3%; Score 760.2; DB 23; Length 1253;
Best Local Similarity 99.6%; Pred. No. 2.2e-207;
Matches 762; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
QY 25 atgtgccagtttcgcatcgtgaagaagtcgcggaagaagacagcggtttgagtcga 84
    |||||||
DB 231 atgtgcagatttcgcatcgtgaagaagtcgcggaagaagacagcggtttgagtcga 290
    |||||||

QY 85 gccgaagtcatcgaagaagcggaagcgcgagcgcggtgtgtgagcccggaagag 144
    |||||||
DB 291 gccgaagtcatcgaagaagcggaagcgcgagcgcggtgtgtgagcccggaagag 350
    |||||||

QY 145 atcgagcggaaggtgagcatccttcggaagtcgcatcaccacaatgcatcacgtcac 204
    |||||||
DB 351 atcgagcggaaggtgagcatccttcggaagtcgcatcaccacaatgcatcacgtcac 410
    |||||||

QY 205 gaagtcatagaacgcgaaccgacgtgtgacatccttcgaagctagtgtcgtgagag 264
    |||||||
DB 411 gaagtcatagaacgcgaaccgacgtgtgacatccttcgaagctagtgtcgtgagag 470
    |||||||

QY 265 ctcttcgatttcctgcgcgcgaagaagatcaactgagtgagagagcgccacagcttcatt 324
    |||||||
DB 471 ctcttcgatttcctgcgcgcgaagaagatcaactgagtgagagagcgccacagcttcatt 530
    |||||||

QY 325 aagcagatcctctgagtcgggtggaataccttcacacaagaagaattgtctactttgattc 384
    |||||||
DB 531 aagcagatcctctgagtcgggtggaataccttcacacaagaagaattgtctactttgattc 590
    |||||||

QY 385 aagcagaaaaacattatgtgtgttagacaagaataatcccatcacaacatcaagctgatt 444
    |||||||
DB 591 aagcagaaaaacattatgtgtgttagacaagaataatcccatcacaacatcaagctgatt 650
    |||||||

QY 445 gaatttgctgtgctcagcaaatagaagatgaggttgtaatttaagaatatatttgagagc 504
    |||||||
DB 651 gaatttgctgtgctcagcaaatagaagatgaggttgtaatttaagaatatatttgagagc 710
    |||||||

QY 505 ccggaattctgtgctcagcaaatgttaactacagagcccttggtctcgtgaagctgacatg 564
    |||||||
DB 711 ccggaattctgtgctcagcaaatgttaactacagagcccttggtctcgtgaagctgacatg 770
    |||||||

QY 565 tggagacatagcgctcatcaactacatccctttaaigtgagacatcccttctcgtgagagc 624
    |||||||
DB 771 tggagacatagcgctcatcaactacatccctttaaigtgagacatcccttctcgtgagagc 830
    |||||||

QY 625 agcgaagcagaagaacactgagcaaatatcacatcagtgaggttaagctttgtagaagattc 684
    |||||||
DB 831 agcgaagcagaagaacactgagcaaatatcacatcagtgaggttaagctttgtagaagattc 890
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QY 685 ttcagcacaacgagcagcgtgagccaagacttaattcgaagctcttcgtttaagaagacc 744
    |||||||
DB 891 ttcagcacaacgagcagcgtgagccaagacttaattcgaagctcttcgtttaagaagacc 950
    |||||||

QY 745 cggaaacggtctacaatccaagaggtctccaagaccccttgatc 789
    |||||||
DB 951 cggaaacggtctacaatccaagaggtctccaagaccccttgatc 995
    |||||||
```

RESULT 3

AAK94258
ID AAK94258 standard; cDNA; 2079 BP.

XX
XX AAK94258;

XX
XX 06-NOV-2001 (first entry)

DE Human full-length cDNA, SEQ ID NO: 2874.

XX
XX Human; full length cDNA; cDNA synthesis; oligo-capping; ss.

```
XX  
OS Homo sapiens.  
XX  
PN EP1130094-A2.  
XX  
PD 05-SEP-2001.  
XX  
PF 07-JUL-2000; 2000EP-0114089.  
XX  
XX 08-JUL-1999; 99JP-0194486.  
PR 11-JAN-2000; 2000JP-0118774.  
PR 02-MAY-2000; 2000JP-0183765.  
XX  
PA (HELI-) HELIX RES INST.  
PI Oka T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y,  
PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;  
XX  
DR WPI: 2001-524255/58.  
DR P-PSDB: AAM93338.  
XX  
XX 830 Primers useful for synthesizing full length cDNA clones and their  
PT use in genetic manipulation -  
PS  
PS Claim 8; SEQ ID NO 2874; 1380bp + sequence listing; English.  
XX  
XX The invention relates to primers for synthesizing full length cDNA  
CC clones. 830 cDNA molecules encoding a human protein have been  
CC isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA  
CC molecules have been determined. Primers for synthesizing the full length  
CC cDNA are useful for clarifying the function of the protein encoded by  
CC the cDNA. The full length clones were obtained by construction of full  
CC length enriched cDNA libraries that were synthesized by the oligo-capping  
CC method. The primers enable the production of the full length cDNA easily  
CC without any special methods. The present sequence is a full length  
CC human cDNA of the invention.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in CD-ROM format directly from EPO.  
XX  
SQ Sequence 2079 BP; 396 A; 626 C; 733 G; 324 T; 0 other;

Query Match 62.8%; Score 495.2; DB 22; Length 2079;  
Best Local Similarity 76.8%; Pred. No. 2.2e-131;  
Matches 605; Conservative 0; Mismatches 183; Indels 0; Gaps 0;



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QY 1 tatgacatcggagagagcgtgtgaggttgccagtttcgcatcgtgaagaagtcgcgagag 60
 |||||
DB 106 tatgagatgggggagagcgtgtgaggttgccagtttcgcatcgtgaagaagtcgcgagag 165
 |||||

QY 61 aagagcacgggcttgatgacagccaagtcatcaagaagcgcgacagcgcgagc 120
 |||||
DB 166 aagagcacgggcttgatgacagccaagtcatcaagaagcgcgacagcgcgagc 225
 |||||

QY 121 cggcgcggtgtgagcgggaagagatcgaggggaggttgagcatccttcggaagtcgagtcgt 180
 |||||
DB 226 cggcgcggtgtgagcgggaagagatcgaggggaggttgagcatccttcggaagtcgagtcgt 285
 |||||

QY 181 caccacaatgtcatcacgctgcagcagctctatgagaacgcgacgcgacgtgtgtcacatc 240
 |||||
DB 286 caccacaatgtcatcacctgcagcagctcttgagaacaagacgcgacgtgtgtccatc 345
 |||||

QY 241 cttagactagtgcttgagaggaagctcttgattcttcgcccagaagagtaactctagtc 300
 |||||
DB 346 cttagactagtgcttgagaggaagctcttgattcttcgcccagaagagtaactctagtc 405
 |||||

QY 301 gagagagagcgaccacgacttcattaaagcagatcctgtgaagggtgaaactacatcacaca 360
 |||||
DB 406 gagagagagcgaccacgacttcattaaagcagatcctgtgaagggtgaaactacatcacatc 465
 |||||

QY 361 aagaanaattgctcaacttgatcatcaagccaagaanaacattatgtgttagacaagaataat 420
 |||||
DB 466 aagcgatcgcgaacacttgacacttgagacgcggaanaacattatcgtcgtgacaagaagacgtg 525
 |||||
```


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proteins and DNA are useful as gene therapeutic agents against cancer, and as anti-cancer agents. The present sequence represents a DNA encoding a

XX
XX

DT 01-JUL-1999 (first entry)


```

OY 1 tatgacatcgagagagctggagagtgccagcttgcacatctgtgaaagaatgccggag 60
   ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 251 tatgagatggggagagagctgggagagcgccagcttgcagctgagcgaagtcggcag 310
OY 61 aagagcaggggcttgagctgacagcaagttcacaagaagcgccagagccggcgagc 120
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 311 aagggcagcgagagagtagcagcagaattcacaagaagcgccgcctgtcaccagc 370
OY 121 cggcgagctgtgagcggagagagatcgagcggagagtgagcactcgcggcaggtctg 180
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 371 cggcgctggggtagcggcgagagatcgagcggagagtgaaacccgcggagatccgg 430
OY 181 caccacagctcatcagcagcgacagcagctctatcagaacccgagcggtgtgacatc 240
   ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 431 caccacacatcatcaccccgacagacatctcgagaacaagacgagcgtgtccatc 490
OY 241 ctggagctagctgtcggagagagagcttcgacttccgtgccagagagagctcagtg 300
   || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 491 ctggagctgtctcgtcgggagagctcttgaactcctcgtcgagagagtgctgacg 550
OY 301 gagagagagcgacacagctcattaaagacatccctgagtggtgtaactcattcaaca 360
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 551 gagagcagggccaccgagctcctcaagacatccctgagcggttcactactcactc 610
OY 361 aagaaatctgctcactctgactctcaagccagaacaacattatgtgttagacaagaatc 420
   ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 611 aagcgactcgacacacttgaactgaagccggaaaacatcatgctgtgaaagaagcgtg 670
OY 421 cccattcacaacacaaagctgattgacttgcgtcgtcagcaagaatagaagagagtt 480
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 671 cccaaacacgaatcagaagctatcagactctcgacatcgccacaagatcggagcgggag 730
OY 481 gaatttaagaatatcttctggagcgccggaattgtctcctcagaagaatgtaactacag 540
   || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 731 gactcagaagacatcttcgcgaccccgaggttctgtgcccagagatctgaaactagag 790
OY 541 cccctggtctgagagctgagcatgtgagcagtagcgctacacactcactcacttaagt 600
   || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 791 ccgctgggctgtgagcgagacatgtgagcatcggtgtcactacattatctcctcagc 850
OY 601 ggaagatccctctcctcgtggagagacagagagaaacatctgcaaatcatcatcagtg 660
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Db 851 ggttcacatcccgctcctcgtggcgagacagagagagcgctcacaacatctcagcgtg 910
OY 661 agttagaacttgaatgaggaattctcagcatcagcgagcggtcgccaagagacttcat 720
   || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 911 aactacagactcgacgagagtagtactcagcaacacccgagcggtcgccaagagactcatt 970
OY 721 cggagagcttctgttaagagagaccggaaacggtcacaatcacaagagcgctcagacac 780
   || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 971 cgcgcgctgtcgtcaaaagatcccaagcggagaaatgacatctgccagagccttgaacat 1030
OY 781 cccctgag 788
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Db 1031 tccctgag 1038

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RESULT 8

AA089839 standard; cDNA; 4272 BP.

XX AA089839;

XX 04-JAN-1980 (first entry)

XX Human death associated protein DAP-2.

XX Death associated protein; DAP; cytokine; cell death; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 1..4272

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FT XX /*tag= a
XX
XX W09510630-A.
XX
XX 20-APR-1995.
XX
XX 12-OCT-1994; 94WO-US11598.
XX
XX 12-OCT-1993; 93IL-0107250.
XX
XX (RYCU/) RYCUS A.
XX (YEDA ) YEDA RES & DEV CO LTD.
XX
XX Kimchi A;
XX
XX WPI; 1995-1/8528/23.
XX
XX P-PSDB; AAR74205.
XX
XX DNA whose expression mediates cytokine-induced programmed cell
XX death - used to treat diseases or disorders associated with
XX uncontrolled, pathological cell growth or cytokine-induced
XX programmed cell death.
XX
XX Claim 2; Fig 8; 61pp; English.
XX
XX DAP genes seem to play an imp. role in programmed cell death and the
XX inhibition of their expression protects the cell from cytokine
XX promoted cell death. A cDNA library was generated from a mixture of
XX mRNAs harvested after treatment of Hela cells with IFN-gamma. It
XX was cloned in antisense orientation into the EBV-based pTK01
XX expression vector. The resulting expression library was introduced
XX into Hela cells. A fraction of the transfectants was selected with
XX hygromycin B. The majority of transfected cells were selected with
XX both hygromycin B and IFN-gamma. The cells that survived and/or
XX grew in the presence of IFN-gamma were expanded and pooled. The
XX extrachromosomal DNA was obt. and cleaved with DpnI and introduced
XX into E. coli HB101 host cells. A few bacterial clones were obt.
XX which included DNA antisense sequences, some of which were able to
XX protect cells from the death-promoting effects of IFN-gamma.
XX Plasmid DNAs were prep. from 10 individual bacterial clones. PCR
XX amplified cDNA inserts were generated from each plasmid using
XX primers that corresp. to the immediate flanking sequence of the
XX cDNA insertion sites in the pTK01 vector. The PCR fragments were
XX used as labeled probes to search Southern blots for possible cross
XX hybridisation between some of the rescued antisense cDNA clones.
XX The 10 cDNA clones were classified into six distinct
XX non-overlapping gps., some constituting several members (clones)
XX and some constituting a single member. Antisense cDNA clone 256 has
XX the DNA product called DAP-2. Clone 256 (DAP-2) was sequenced and
XX used to screen a K562 lambda gt10 cDNA library. The resulting
XX composite sequence derived from 2 clones and the deduced AA sequence
XX are shown in AA089838 and AAR74205. The ORF is also shown in AA089839.
XX AA089838 has a poly A tail. The calculated mol. wt. of the protein
XX is about 160 kDa. Several known domains and motifs were identified
XX in the protein (see AA074205 FT).
XX
XX Sequence 4272 BP; 1076 A; 1161 C; 1121 G; 914 T; 0 other;
XX
XX Query Match 50.5%; Score 398.2; DB 16; Length 4272;
XX Best Local Similarity 70.6%; Pred. No. 1,86-103;
XX Matches 557; Conservative 0; Mismatches 208; Indels 24; Gaps 1;
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OY 61 aagagcaggggcttgagctgacagcaagttcacaagaagcgccagagccggcgagc 120
   || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 97 aaaagtacgggcttcacgactcccgcaaatcacaagaagagactcaaatccagc 156
   || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 121 cggcgagctgtgagccggagagatcgagcggagagtgagcatccctgagcaggtctg 180
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Db 157 cggcggtgtgtgagcgcgagagacatcgagcggaggttcagcatcctgaagagatccag 216
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Db 217 caccacaatgtatcatcacccttcgacgagctcatgagaacgaagcagcagctcatcctgac 276
Oy 241 ctgagctagtgtctgtgaggaagctctcgaatttcctgtcccaagaagagctgactgagt 300
Db 277 ttggaactcgtgtgaggtgagcagctgtgtgactctcttgatgcgaaagaagatcttaact 336
Oy 301 gagggaggggcccacagctctcatatgaagacatccctgagtggtgtgaactcctacaca 360
Db 337 gaagaggaagcaactggaattctcacaacaaattctaattgtgttactactgacatcc 396
Oy 361 aagaattgtcactcttgatctcatcgaagccgaacaaatattgtttgtagacaagaattat 420
Db 397 ctccaatccgccaactttgatcttaagcctgagacaataagcttcttgatagaatagtc 456
Oy 421 cccattccacacataaagctgtgacttggctgtcgtcagaaatagaaatgagtt 480
Db 457 cccaactcgtgataagaatcatgactt-----tggaat 492
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Oy 781 cccctgagatc 789
Db 793 cccctgagatc 801

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RESULT 9

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AA089838
ID AA089838 standard; cDNA; 5886 BP.
XX
AC AA089838;
XX
DT 04-JAN-1980 (first entry)
XX
DE Human death associated protein DAP-2.
XX
KW Death associated protein; DAP; cytokine; cell death; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 337..4605
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FT /note= "claimed"
FT polyA_signal 5628..5633
FT /tag= b
FT polyA_signal 5855..5860
FT /tag= c
FT misc_feature 5114..5118
FT /tag= d
FT /label= instability motif
FT misc_feature 5103..5107

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FT FT /tag= e
FT FT /label= instability motif
PN PN
XX MO9510630-A.
XX
PD 20-APR-1995.
XX
PF 12-OCT-1994; 94MO-US11598.
XX
PR 12-OCT-1993; 93IL-0107250.
XX
PA (RYCUS/) RYCUS A.
PA (YEDA) YEDA RES & DEV CO LTD.
XX
PI Kimchi A;
XX
DR WPI. 1995-178528/23.
XX
DR P-PSDB; AAR74205.
XX
PT DNA whose expression mediates cytokine-induced programmed cell
PT death - used to treat diseases or disorders associated with
PT uncontrolled, pathological cell growth or cytokine-induced
PT programmed cell death.
XX
PS Claim 2; Fig 8; 61pp; English.
XX
CC DAP genes seem to play an imp. role in programmed cell death and the
CC inhibition of their expression protects the cell from cytokine-
CC promoted cell death. A cDNA library was generated from a mixture of
CC mRNAs harvested after treatment of HeLa cells with IFN-gamma. It
CC was cloned in antisense orientation into the EBV-based pTK01
CC expression vector. The resulting expression library was introduced
CC into HeLa cells. A fraction of the transfectants was selected with
CC hygromycin B. The majority of transfected cells were selected with
CC both hygromycin B and IFN-gamma. The cells that survived and/or
CC grew in the presence of IFN-gamma were expanded and pooled. The
CC extrachromosomal DNA was obtd. and cleaved with DpnI and introduced
CC into E. coli HB101 host cells. A few bacterial clones were obtd.
CC which included DNA antisense sequences, some of which were able to
CC protect cells from the death-promoting effects of IFN-gamma.
CC Plasmid DNAs were prepd. from 10 individual bacterial clones. PCR
CC amplified cDNA inserts were generated from each plasmid using
CC primers that corresp. to the immediate flanking sequence of the
CC cDNA insertion sites in the pTK01 vector. The PCR fragments were
CC used as labeled probes to search Southern blots for possible cross
CC hybridisation between some of the rescued antisense cDNA clones.
CC The 10 cDNA clones were classified into six distinct
CC non-overlapping gps., some constituting several members (clones)
CC and some constituting a single member. Antisense cDNA clone 256 has
CC the DNA product called DAP-2. Clone 256 (DAP-2) was sequenced and
CC used to screen a K562 lambda gt10 cDNA library. The resulting
CC composite sequence derived from 2 clones and the deduced AA sequence
CC are shown in AA089838 and AAR74205. The ORF is also shown in AA089839.
CC AA089838 has a poly A tail. The calculated mol. wt. of the protein
CC is about 160 kDa. Several known domains and motifs were identified
CC in the protein (see AA074205 FT).
XX
SQ Sequence 5886 BP; 1447 A; 1524 C; 1500 G; 1415 T; 0 other:

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Query Match 50.5%; Score 398.2; DB 16; Length 5886;
Best Local Similarity 70.6%; Pred. No. 2,1e-103;
Matches 557; Conservative 0; Mismatches 208; Indels 24; Gaps 1;

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Oy 1 tatgacatcgcgagagagctggtgggtgtgcccagttgcatcgttgaagaagtcggggag 60
Db 373 taagacacgcgcgaggaacttggcagtgacagcttgcgtgtggaagaatgacgttgag 432
Oy 61 aagagcacggggctgagatgcagcaagttcatcaaaagcggcagagccggggagc 120
Db 433 aaagttaccggtcctcagtatccgcacaaattcatcaagaaagagagcctaagtcacg 492
Oy 121 cggcggtgtgtgagcgcgagagagatcgagcggaggtgagacatcctcgtcagagtgctg 180

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D	493	cgcgcggggtgtgtgcccgcgagagacacgcgagcgggaggtlcaagatccctctgaagagagatccag	552
Q	181	caccacaatgtcatcaccgtctcagcagcagcgtctatgtgaaccgcgcacgcagcgtgtgtgcacat	240
D	553	caccaccaatgtcatcaccgtctcagcagcagcgtctatgtgaagacaagacgacgtcatccgtac	612
Q	241	cttgagatgtgtgtctgtgagagagagccttcgcattccctcgtgcccagaagagatcaactgagt	300
D	613	ctggaaactcgtctcaggtgtgcgagcgtgttgcattccttcgtgcgaagaagaaacttctaact	672
Q	301	gagagagagagcgcacccagcttcattaaagcagatccctgtgagtggtgtgaacttaccatcaaca	360
D	673	gagagagagagcgcacccagcttcattaaagcagatccctgtgagtggtgtgaacttaccatcc	732
Q	361	aagagaatatgtctactcttgatctcaacgcagacgaagaacatattgtgtltagaagaataatt	420
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D	793	cccaaaacctcgtgacaaagatcatgtgact-----tggaat	828
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D	829	gaatttaagaatatcttcttgagagccggaattgtgtccagaatatgtgaactacagag	888
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D	889	ccccctgtctctgagagcctgcacgtgtgagacatagcgtcatcaccatcacccttaagt	948
Q	601	ggagacatccctctcctcgtgagacacgagacgaagaacatctgcacaatalcatcacatcagtg	660
D	949	ggggccctcccatcttctcttgagacactaaagcaagaacgttagcaatgtatccgtctc	1008
Q	661	agttacgactttgatgaggaattcttcagccatacagagcagagcgtgccaaggaacttaatt	720
D	1009	aactacgaatttgatgagatgcattctcagtaataccaggtgcccttagccaaagaatttcata	1068
Q	721	cgagagctctgtgttaagaagaccgcggaacggtccacacatccaaagagccttcagacac	780
D	1069	agaaagactctctgtcacaagatcccaagaagagaaatgacatcaagaatagtttgcagcat	1128
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AAV60289 standard; DNA; 5886 BP.			
AAV60289:			
12-JAN-1999 (first entry)			
DNA sequence encoding death associated protein-2 (DAP-1, DAP-kinase).			
KW	Death associated protein; DAP-2; cell death; tumour cell; DAP-kinase;		
KW	metastatic activity; cancer; psoriasis; autoimmune disease;		
KW	Programmed cell death; degenerative neurological disease;		
KW	Alzheimer's; ss.		
OS	Homo sapiens.		
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FX	Key	Location/Qualifiers	
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FT		/*tag= a	
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XX	W09839429-A2.		
XX	11-SEP-1998.		
XX			

PF	03-MAR-1998;	98WO-IL00102.		
XX				
XX	03-MAR-1997;	97US-0810712.		
XX				
PA	(YEDA)	YEDA RES & DEV CO LTD.		
XX				
PI	Kimchi A:			
XX				
DR	WPI: 1998-520781/44.			
DR	P-PSDB: AAM71367.			
XX				
PT	New isolated death associated protein nucleic acids - used for the			
PT	diagnosis and treatment or disorders associated with programmed cell			
PT	death, e.g. cancers, auto-immune disease or neurological disease			
XX				
PS	Claim 2; Fig 8; 157pp: English.			
XX				
CC	The present sequence encodes a death associated protein-2 (DAP-2,			
CC	DAP-Kinase). The DAP genes and proteins are used for promoting death of			
CC	normal or tumour cells, and for suppressing the metastatic activity of			
CC	tumour cells. They can be used in the treatment of diseases or disorders			
CC	associated with uncontrolled pathological growth, e.g. cancer,			
CC	psoriasis, autoimmune diseases and others. Agents which antagonise,			
CC	inhibit or neutralize DAP products are used for protecting cells from			
CC	programmed cell death. In this case they can be used for the treatment			
CC	of degenerative neurological diseases, e.g. Alzheimer's, prevention of			
CC	death of T cells in AIDS patients, prevention of rejection associated			
CC	cell death in transplants, and protection of normal cells from			
CC	the cytotoxic effects of anti-cancer therapies.			
XX				
XX	Sequence 5886 BP; 1447 A; 1525 C; 1499 G; 1415 T; 0 other:			
SO				
Query Match				
Best Local Similarity 50.5%; Score 398.2; DB 19; Length 5886;				
Matches 557; Conservative 70.6%; Pred. No. 2.1e-103; Indels 24; Gaps 1				
QY	1	tatgacatcgagagagagcttggtggaagtgcacagttgcatcgttgaagaagtcgagag 60		
DB	373	tacgacacgcggaggaacttgcgcagtgcagcgttttcggttgcgtgaagaagtcgagag 432		
QY	61	aagagcacggggtcttgatgatacgacccaagtcatcaagaagcggcagagccgggcgagc 120		
DB	433	aaagtacgcgcctccagatccgcgaattcatcaagaagaagagactaagtcacgc 492		
QY	121	cggcgcggtgtgaagccggagagatcgacggcgagggtgtagatcctcgcgcagtgctgcg 180		
DB	493	cggcgagggtgtgagcgcgcgagagacatcgagcgggaggttcagatcctcgaaggatccag 552		
QY	181	caccacatgtatatacgcgttcagacagcgtctcttgagaacgcgacgcagctgtgtgcacac 240		
DB	553	caccccaatgcatcacccctgcgcagaggtcctatgagaaagaacggaagtcacatcctgacac 612		
QY	241	cttgacatgctgtcctcgagggagagctcttcgaattccctcgtgccagagagagtcactgaat 300		
DB	613	ttgagacccgtgtcagagtggtgcgactgtgttgactctcttaagtcgaaaggaatccttaact 672		
QY	301	gagagagggccacacagctcataaagacagatcctgtagtggtgtgaactacctaacaaca 360		
DB	673	gaagaggaagcacatgaatttctcaacaacaattcttaagtggttactactcctgacatcc 732		
QY	361	aagaaatgtgcactttgcatctgaatcgaagccagaaacatatattgtttgaagaagaattat 420		
DB	733	cttcaaatcgcgccacttgcattcctaagcccgagacaataaagcttcttgatagaatgctc 792		
QY	421	cccatctcaacacataaagctgattgaacttggctcgtgcacgaagaatagaatgagatt 480		
DB	793	cocaaactcgtgatacaagatcatgaactt-----tggaaat 828		
QY	481	gaatttaagaatatttttgagagccgcggaatttgtctgcagaaattgtgactaagag 540		
DB	829	gaatttaaaaaaatatttttgagatccagaggtttgcgcctccgagataatcaacataatga 888		

08-JUL-1999; 99JP-0194486.
11-JAN-2000; 2000JP-0118774.

XX (HELI-) HELIX RES INST.
PA
XX Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX WPI: 2001-524255/58.
DR
XX
PT 830 Primers useful for synthesizing full length cDNA clones and their
PT use in genetic manipulation -
PS
PS Example 11: SEQ ID NO 1722: 1380bp + sequence listing: English.
XX
CC The invention relates to primers for synthesizing full length cDNA
CC clones. 830 cDNA molecules encoding a human protein have been
CC isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA
CC molecules have been determined. Primers for synthesizing the full length
CC cDNA are useful for clarifying the function of the protein encoded by
CC the cDNA. The full length clones were obtained by construction of full
CC length enriched cDNA libraries that were synthesised by the oligo-capping
CC method. The primers enable the production of the full length cDNA easily
CC without any special methods. The present sequence was used in
CC representative sequence from a human clone which was used in
CC homology searches to identify the clone.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in CD-ROM format directly from EPO.
XX
XX Sequence 757 BP; 176 A; 219 C; 220 G; 133 T; 9 other;

Query Match 46.5%; Score 366.6; DB 22; Length 757;
Best Local Similarity 75.9%; Pred. No. 8.7e-95;
Matches 486; Conservative 0; Mismatches 151; Indels 3; Gaps 3;

QY 1 tatgacatcgagagagctgggagctggcagcttgccatcgtgaagaagtcgaggag 60
DB 106 tatgagctgggagagctggcagcttgccatcgttgagcgtgaggaagtcgaggag 165
QY 61 aagagacaggggcttgatataagcacaagtcatacaagaagcgcgagcgagc 120
DB 166 aaggacaggggcaagaagctacgacagtcacaaagtcgagcgcgctgacacgc 225
QY 121 cgggagctgtagcgggagagatcgagcggaggtgagatccttcgagctgctg 180
DB 226 cggcgtggggtgagcgggagagatcgagcggaggtgagatccttcgagctgctg 285
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DB 466 aagcagctgcacactctgacttcgaagccgaagaaacatgatgtgttgacaagaagc 525
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QY 599 gtgagacat-cccccttcctgggagacatcgaagcagaa 637
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ID AAK70641 standard: DNA; 12638 BP.
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AC AAK70641;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human Immune/Haematopoietic antigen genomic sequence SEQ ID NO:25453.
XX
KW Human; Immune; haematopoietic; Immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.
OS Homo sapiens.
XX
PN WO200157182-A2.
PD
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XX 09-AUG-2001.
PE 17-JAN-2001; 2001WO-US01354.
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XX 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226861.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0228287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
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PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
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PR 05-JAN-2001; 2000US-0254097.
PR 05-JAN-2001; 2000US-0259678.
PR (HUMA-) HUMAN GENOME SCI INC.
PR PA
PR XX
PR XX
PI Rosen CA, Barash SC, Ruben SM.
PI XX
DR WPI: 2001-483426/52.
XX
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and
PT metastasis -
PS
PS Disclosure: SEQ ID NO 25453; 3071pp + Sequence Listing: English.
XX
XX AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
CC amino acid sequences given in AAK62170 to AAK61921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patient's own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/hematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/hematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
CC represent sequences used in the exemplification of the present invention.
XX
SQ Sequence 12638 BP; 2397 A; 3383 C; 3994 G; 2864 T; 0 other;

Query Match 31.0%; Score 244.6; DB 22; Length 12638;
Best Local Similarity 79.6%; Pred No. 36-59;
Matches 289; Conservative 0; Mismatches 74; Indels 0; Gaps 0;
QY 25 agtggcagttgtccatcgtgaagaagttccgggagaagacgggggtctgagatgca 84
DB 6096 agcggcagttgtcgatcgtgcaagttccgggacgaaggcggcggaaggatcgca 6155
QY 85 gccaaagttcatcaagaagcggcgagagcggcgcgagcggcggtgtgagccggagag 144
DB 6156 gccaaagttcatcaagaagcggcgatccatccagcggcggtgtgagccggagag 6215
QY 145 atcgaagcggaggtgtgacatcctcgcgcgaggtgtgtcacacaatgtcatcaagctgcac 204
DB 6216 atcgaagcggaggtgtgaacatcctcgcgcgaggtgtgtcacacaatgtcatcaagctgcac 6275
QY 205 gacgtctatgagaacccgcagcgtgtgacacatccttgagtagtgtctgagagagag 264
DB 6276 gacatctcgagaacaagcagcgtgtgtccatccatccttgagtagtgtctgagagagag 6335
QY 265 ctcttcgattcctggcccaagaagagtagtactagtgagagagagccacacattcat 324
||||| ||| ||||||| ||||||| ||||| ||||||| ||||| |||

Db 6336 cctcttgactctcgtgcggaagaagctgcctgacgagagagcagccaccagttcttc 6395
QY 325 aagcagatccctggtatcggtgaaactcctcacacaagaattgctcattgattc 384
Db 6396 aagcagatccctggtgaaactcctcacacaagaattgctcattgattc 6455
QY 385 aag 387
Db 6456 aag 6458

RESULT 14
ABAO9608
ID ABA09608 standard; DNA: 1120 BP.
AC ABA09608;
XX
XX 15-JAN-2002 (first entry)
DE Human bone marrow expressed oligonucleotide SEQ ID NO: 34.
XX
XX Human: bone marrow; cytostatic; antirheumatic; antiarthritic; vulnery;
KW antinflammatory; antibacterial; immunosuppressive; vasotropic; cancer;
KW antiparkinsonian; neuroprotective; nootropic; haemostatic; osteopathic;
KW antilicer; fungicide; antidiabetic; antiasthmatic; antiallergic;
KW immunostimulant; analgesic; cerebroprotective; antianaemic; infection;
KW nervous system disorder; autoimmune disorder; inflammation; allergy; ds.
XX
XX Homo sapiens.
OS
XX WO200174836-A1.
PN
XX 11-OCT-2001.
PD
XX 30-MAR-2001; 2001WO-US10472.
PE
XX 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
PR 23-AUG-2000; 2000US-0649267.
PR 30-NOV-2000; 2000US-250583P.
XX
XX (HYSE-) HYSEQ INC.
PA
XX Tang YT, Liu C, Drmanac RT, Ford JE, Boyle BJ;
PI
XX WPI: 2001-626375/72.
DR P-PSDB; ABB12364.
DR
XX New bone marrow-expressed nucleic acids and polypeptides, useful for
PT diagnosis, treatment of inflammatory, autoimmune, neurological, cancer
PT and increasing hematopoiesis, stem cell survival and bone growth and
PT remodeling
XX
XX Claim 1; Page 182; 380pp; English.
PS
XX The present invention relates to bone marrow expressed polynucleotides
CC and proteins. These sequences can be used in the treatment of
CC inflammatory conditions (eg arthritis, Crohn's disease), cancer, central
CC and peripheral nervous system diseases and neuropathies, such as
CC Alzheimer's, Parkinson's and Huntington's diseases, spinal cord
CC disorders, head trauma, cerebrovascular diseases, myeloid and lymphoid
CC cell disorders, platelet disorders, stem cell disorders, bone
CC degenerative disorders, autoimmune disorders, for example multiple
CC sclerosis, diabetes and arthritis, viral and bacterial infections,
CC allergies and blood coagulation disorders. The present sequence is a DNA
CC of the invention.
XX
XX Sequence 1120 BP; 271 A; 304 C; 315 G; 230 T; 0 other;

Query Match 29.0%; Score 228.8; DB 22; Length 1120;
Best Local Similarity 96.8%; Pred. No. 3e-55;
Matches 244; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY 539 agcccttggtctggaagctgacatgtgtgacataagcgtcatcattactactcttaa 598
Db 23 agcccttggtctggaagctgacatgtgtgacataagcgtcatcattactactcttaa 82
QY 599 gtgagacatccctctctctggaagacaggaagacactggaataatcacacag 658
Db 83 gtgagacatccctctctctggaagacaggaagacactggaataatcacacag 142
QY 659 tgaattacgacttgatgaagaaattctcagc-catacgagagctggtccaaagactt 717
Db 143 tgaattacgacttgatgaagaaattctcagcagcagagcgtggtccaaagactt 202
QY 718 attcggaaagcttctggttaagaagaccggaaagcgtcacaatccaaagagcttaca 777
Db 203 attcggaaagcttctggttaagaagaccggaaagcgtcacaatccaaagagcttaca 262
QY 778 cacccttgatc 789
Db 263 cacccttgatc 274

RESULT 15
ABAO9692
ID ABA09692 standard; DNA: 1505 BP.
AC ABA09692;
XX
XX 15-JAN-2002 (first entry)
DE
XX Human bone marrow expressed oligonucleotide SEQ ID NO: 201.
XX
XX
XX Human: bone marrow; cytostatic; antirheumatic; antiarthritic; vulnery;
KW antinflammatory; antibacterial; immunosuppressive; vasotropic; cancer;
KW antiparkinsonian; neuroprotective; nootropic; haemostatic; osteopathic;
KW antilicer; fungicide; antidiabetic; antiasthmatic; antiallergic;
KW immunostimulant; analgesic; cerebroprotective; antianaemic; infection;
KW nervous system disorder; autoimmune disorder; inflammation; allergy; ds.
XX
XX Homo sapiens.
OS
XX WO200174836-A1.
PN
XX 11-OCT-2001.
PD
XX 30-MAR-2001; 2001WO-US10472.
PE
XX 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
PR 23-AUG-2000; 2000US-0649267.
PR 30-NOV-2000; 2000US-250583P.
XX
XX (HYSE-) HYSEQ INC.
PA
XX Tang YT, Liu C, Drmanac RT, Ford JE, Boyle BJ;
PI
XX WPI: 2001-626375/72.
DR
XX New bone marrow-expressed nucleic acids and polypeptides, useful for
PT diagnosis, treatment of inflammatory, autoimmune, neurological, cancer
PT and increasing hematopoiesis, stem cell survival and bone growth and
PT remodeling
XX
XX Claim 1; Page 276-277; 380pp; English.
PS
XX The present invention relates to bone marrow expressed polynucleotides
CC and proteins. These sequences can be used in the treatment of
CC inflammatory conditions (eg arthritis, Crohn's disease), cancer, central
CC and peripheral nervous system diseases and neuropathies, such as
CC Alzheimer's, Parkinson's and Huntington's diseases, spinal cord
CC disorders, head trauma, cerebrovascular diseases, myeloid and lymphoid
CC cell disorders, platelet disorders, stem cell disorders, bone
CC degenerative disorders, autoimmune disorders, for example multiple

CC sclerostis, diabetes and arthritis, viral and bacterial infections,
CC allergies and blood coagulation disorders. The present sequence is a DNA
CC of the invention.

XX
SQ Sequence 1505 BP; 417 A; 355 C; 399 G; 334 T; 0 other;

Query Match 29.0%; Score 228.8; DB 22; Length 1505;
Best Local Similarity 96.8%; Pred. No. 3.5e-55;
Matches 244; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

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Db 23 agccctgagctcgagagctgacatgtgagatagggcgtcatcactcatcctctta 82
   |||||
OY 599 gtgagacatcccttctctctgagagacagaaagcaaacactggaataatcacatcag 658
   |||||
Db 83 gtgagacatcccttctctctgagagacagaaagcaaacactggaataatcacatcag 142
   |||||
OY 659 tgaattacgacttgaatgagaatctctcagc-catacagcgagctgccaaggacttt 717
   |||||
Db 143 tgaattacgacttgaatgagaatctctcagc-catacagcgagctgccaaggacttt 202
   |||||
OY 718 attcggaagcttctgttaagaagaccggaacggctcacatccaagaaggctctcaga 777
   |||||
Db 203 attcggaagcttctgtgttaagaagaccggaacggctcacatccaagaaggctctcaga 262
   |||||
OY 778 cacccttgatc 789
   |||||
Db 263 cacccttgatc 274
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